

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 101527,571A  
Source: IPGIO  
Date Processed by STIC: 8/22/06

***ENTERED***



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/527,571A

DATE: 08/22/2006  
TIME: 11:14:39

Input Set : N:\RJAVED\10527571.txt  
Output Set: N:\CRF4\08222006\J527571A.raw

3 <110> APPLICANT: Syngenta Participations AG  
4 Stam, Lynn  
5 Kamdar, Kim  
6 Spana, Eric  
7 Bachmann, Jane  
9 <120> TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that  
Encode Proteins  
10 Essential for Viability and Uses Thereof  
12 <130> FILE REFERENCE: 70131USPCT  
14 <140> CURRENT APPLICATION NUMBER: US/10/527,571A  
15 <141> CURRENT FILING DATE: 2005-03-14  
17 <150> PRIOR APPLICATION NUMBER: 60/422,377  
18 <151> PRIOR FILING DATE: 2002-10-29  
20 <160> NUMBER OF SEQ ID NOS: 381  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 27  
26 <212> TYPE: DNA  
27 <213> ORGANISM: artificial sequence  
29 <220> FEATURE:  
30 <221> NAME/KEY: misc\_feature  
31 <222> LOCATION: (1)..(27)  
32 <223> OTHER INFORMATION: primer Plac4  
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36 actgtgcgtt aggtcctgtt cattgtt 27  
39 <210> SEQ ID NO: 2  
40 <211> LENGTH: 24  
41 <212> TYPE: DNA  
42 <213> ORGANISM: artificial sequence  
44 <220> FEATURE:  
45 <221> NAME/KEY: misc\_feature  
46 <222> LOCATION: (1)..(24)  
47 <223> OTHER INFORMATION: Primer Plac1  
50 <400> SEQUENCE: 2  
51 cacccaaggc tctgctccca caat 24  
54 <210> SEQ ID NO: 3  
55 <211> LENGTH: 23  
56 <212> TYPE: DNA  
57 <213> ORGANISM: artificial sequence  
59 <220> FEATURE:  
60 <221> NAME/KEY: misc\_feature  
61 <222> LOCATION: (1)..(23)  
62 <223> OTHER INFORMATION: Primer Pry4  
65 <400> SEQUENCE: 3

file:///C:/CRF4/Outhold/VsrJ527571A.htm

8/22/2006

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66 caatcatatc gctgtctcac tca	23
69 <210> SEQ ID NO: 4	
70 <211> LENGTH: 26	
71 <212> TYPE: DNA	
72 <213> ORGANISM: artificial sequence	
74 <220> FEATURE:	
75 <221> NAME/KEY: misc_feature	
76 <222> LOCATION: (1)..(26)	
77 <223> OTHER INFORMATION: Primer Pry1	
80 <400> SEQUENCE: 4	
81 ccttagcatg tccgtgggt ttgaat	26
84 <210> SEQ ID NO: 5	
85 <211> LENGTH: 28	
86 <212> TYPE: DNA	
87 <213> ORGANISM: artificial sequence	
89 <220> FEATURE:	
90 <221> NAME/KEY: misc_feature	
91 <222> LOCATION: (1)..(28)	
92 <223> OTHER INFORMATION: Primer Pry2	
95 <400> SEQUENCE: 5	
96 ctgcccgacg ggaccacctt atgttatt	28
99 <210> SEQ ID NO: 6	
100 <211> LENGTH: 19	
101 <212> TYPE: DNA	
102 <213> ORGANISM: artificial sequence	
104 <220> FEATURE:	
105 <221> NAME/KEY: misc_feature	
106 <222> LOCATION: (1)..(19)	
107 <223> OTHER INFORMATION: Primer Plw3-1	
110 <400> SEQUENCE: 6	
111 tgtcggcgtc atcaactcc	19
114 <210> SEQ ID NO: 7	
115 <211> LENGTH: 29	
116 <212> TYPE: DNA	
117 <213> ORGANISM: artificial sequence	
119 <220> FEATURE:	
120 <221> NAME/KEY: misc_feature	
121 <222> LOCATION: (1)..(29)	
122 <223> OTHER INFORMATION: Primer Pwht1	
125 <400> SEQUENCE: 7	
126 gtaacgctaa tcactccgaa caggtcaca	29
129 <210> SEQ ID NO: 8	
130 <211> LENGTH: 25	
131 <212> TYPE: DNA	
132 <213> ORGANISM: artificial sequence	
134 <220> FEATURE:	
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136 <222> LOCATION: (1)..(25)	
137 <223> OTHER INFORMATION: Primer Splac2	

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140 <400> SEQUENCE: 8
141 gaattcactg gccgtcggtt tacaa 25
144 <210> SEQ ID NO: 9
145 <211> LENGTH: 22
146 <212> TYPE: DNA
147 <213> ORGANISM: artificial sequence
149 <220> FEATURE:
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151 <222> LOCATION: (1)..(22)
152 <223> OTHER INFORMATION: Primer Sp1
155 <400> SEQUENCE: 9
156 acacaacctt tcctctcaac aa 22
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 24
161 <212> TYPE: DNA
162 <213> ORGANISM: artificial sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)..(24)
167 <223> OTHER INFORMATION: Primer Sp3
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171 gagtacgcaa agcttaact atgt 24
174 <210> SEQ ID NO: 11
175 <211> LENGTH: 23
176 <212> TYPE: DNA
177 <213> ORGANISM: artificial sequence
179 <220> FEATURE:
180 <221> NAME/KEY: misc_feature
181 <222> LOCATION: (1)..(23)
182 <223> OTHER INFORMATION: Primer Sp6
185 <400> SEQUENCE: 11
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190 <211> LENGTH: 25
191 <212> TYPE: DNA
192 <213> ORGANISM: artificial sequence
194 <220> FEATURE:
195 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (1)..(25)
197 <223> OTHER INFORMATION: Primer Sp5
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204 <210> SEQ ID NO: 13
205 <211> LENGTH: 19
206 <212> TYPE: DNA
207 <213> ORGANISM: artificial sequence
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: (1)..(19)

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Input Set : N:\RJAVED\10527571.txt  
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212 <223> OTHER INFORMATION: Primer Spep1  
 215 <400> SEQUENCE: 13  
 216 gacactcaga atactattc 19  
 219 <210> SEQ ID NO: 14  
 220 <211> LENGTH: 6342  
 221 <212> TYPE: DNA  
 222 <213> ORGANISM: Drosophila melanogaster  
 224 <220> FEATURE:  
 225 <221> NAME/KEY: CDS  
 226 <222> LOCATION: (1)..(6342)  
 227 <223> OTHER INFORMATION: CT28483  
 230 <400> SEQUENCE: 14  
 231 atg acc gcc tcg gat aaa tac acg tac cag cgg acc gtt ctc tgc ctg 48  
 232 Met Thr Ala Ser Asp Lys Tyr Thr Tyr Gln Arg Thr Val Leu Cys Leu  
 233 1 5 10 15  
 235 gcc cgc gtt ctg gcg ggc atc cag ccc act ccc tgg gat aag gta cat 96  
 236 Ala Arg Val Leu Ala Gly Ile Gln Pro Thr Pro Trp Asp Lys Val His  
 237 20 25 30  
 239 gtc cac ctg gcc acc cac tcc acc agc cac agc gcc agc ccc cct ggc 144  
 240 Val His Leu Ala Thr His Ser Thr Ser His Ser Ala Ser Pro Pro Gly  
 241 35 40 45  
 243 aat cga ctt ttc gca ctg acc ttg agc ggc cat aaa aca gac atg 192  
 244 Asn Arg Leu Phe Ala Leu Thr Leu Ser Gly Gly His Lys Thr Asp Met  
 245 50 55 60  
 247 cgt ggg cgc tca ggg ggc ggt aag gca gtg cag acc ctg ttc cgg 240  
 248 Arg Gly Arg Ser Gly Gly Lys Ala Val Gln Thr Leu Phe Arg  
 249 65 70 75 80  
 251 tat tgt ccg cag gag aat gct gcc gga gtg ttt tgc ctg gac acg cgg 288  
 252 Tyr Cys Pro Gln Glu Asn Ala Ala Gly Val Phe Cys Leu Asp Thr Arg  
 253 85 90 95  
 255 gcc cag gat gcc gta att gcg ctg ggc att tat ttt ctg gag ggc ggc 336  
 256 Ala Gln Asp Ala Val Ile Ala Leu Gly Ile Tyr Phe Leu Glu Gly  
 257 100 105 110  
 259 tgc cag cac gag ggc cag att gtg ccc tat ctg ctg cgt ctg gcc aag 384  
 260 Cys Gln His Glu Gly Gln Ile Val Pro Tyr Leu Leu Arg Leu Ala Lys  
 261 115 120 125  
 263 tgt ctg ccg aag gcg gtc tgg att gac gat gcc cgg agc aac aaa gtg 432  
 264 Cys Leu Pro Lys Ala Val Trp Ile Asp Asp Ala Arg Ser Asn Lys Val  
 265 130 135 140  
 267 gaa cgc gtt cgc att ccg tcg gcg gaa aag ttc agc ttc tgc ttg aac 480  
 268 Glu Arg Val Arg Ile Pro Ser Ala Glu Lys Phe Ser Phe Cys Leu Asn  
 269 145 150 155 160  
 271 acc ctg ctg tcc gac ata gcg gcc aag tgt ccg gat tcg cgc gag gag 528  
 272 Thr Leu Leu Ser Asp Ile Ala Ala Lys Cys Pro Asp Ser Arg Glu Glu  
 273 165 170 175  
 275 atc atc ctg aat cag gtg gaa acg ctg agc gcg ctg gcc aac ata gtc 576  
 276 Ile Ile Leu Asn Gln Val Glu Thr Leu Ser Ala Leu Ala Asn Ile Val  
 277 180 185 190  
 279 aag tcg agc agg gac agc agc tcc gca ccg ccc atc atc ctg tgc 624

RAW SEQUENCE LISTING  
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280	Lys	Ser	Ser	Arg	Asp	Ser	Ser	Ala	Pro	Pro	Pro	Ile	Ile	Leu	Cys		
281		195				200						205					
283	aag	gcc	acg	gtg	ccg	ctg	ctc	ttc	ggc	ttg	gcg	cga	tcg	atg	ggt	cgc	672
284	Lys	Ala	Thr	Val	Pro	Leu	Leu	Phe	Gly	Leu	Ala	Arg	Ser	Met	Gly	Arg	
285			210				215				220						
287	tat	gcc	agc	aac	gat	cca	ccg	ctg	ctg	tcg	cgc	att	ttt	ccg	ccc	gag	720
288	Tyr	Ala	Ser	Asn	Asp	Pro	Pro	Leu	Leu	Cys	Arg	Ile	Phe	Pro	Pro	Glu	
289	225					230				235			240				
291	ctg	ctg	ccc	atc	cag	aag	ggc	ggc	ggc	cgc	gac	ggc	acc	ggc	tcg	agc	768
292	Leu	Leu	Pro	Ile	Gln	Lys	Gly	Gly	Gly	Arg	Asp	Gly	Thr	Gly	Ser	Ser	
293				245				250			255						
295	agc	agt	gcc	agc	ggc	acc	tgc	ggc	ggc	tcc	ttc	agc	agc	agc	gaa	cgc	816
296	Ser	Ser	Ala	Ser	Gly	Thr	Cys	Gly	Gly	Ser	Phe	Ser	Ser	Ser	Glu	Arg	
297						260			265			270					
299	ctg	gcf	gcc	acg	cat	cac	ttc	cga	ccc	atc	ata	ccg	cgc	tcc	atg	tcc	864
300	Leu	Ala	Ala	Thr	His	His	Phe	Arg	Pro	Ile	Ile	Pro	Arg	Ser	Met	Ser	
301				275			280			285							
303	ggc	agt	ctg	gcf	cag	gcc	cag	aac	gca	agc	tac	gac	gat	gga	agg	cag	912
304	Gly	Ser	Leu	Ala	Gln	Ala	Gln	Asn	Ala	Ser	Tyr	Asp	Asp	Gly	Arg	Gln	
305	290				295				300								
307	cgf	tgc	gcf	ggc	ggc	aag	ccc	agc	aag	cca	tcg	ttg	cac	agc	tac	ttt	960
308	Arg	Cys	Ala	Gly	Gly	Lys	Pro	Ser	Lys	Pro	Ser	Leu	His	Ser	Tyr	Phe	
309	305					310				315			320				
311	tcg	gtg	ccg	tac	gat	ccg	cgf	acg	cac	ttc	ttc	acg	cgc	tac	ggc	tcc	1008
312	Ser	Val	Pro	Tyr	Asp	Pro	Arg	Thr	His	Phe	Phe	Thr	Arg	Tyr	Gly	Ser	
313				325				330			335						
315	agt	tgc	aac	caa	ttc	ccg	aac	atg	cgc	gtc	tgc	gaa	tcg	ccc	acg	aaa	1056
316	Ser	Phe	Asn	Gln	Phe	Pro	Asn	Met	Arg	Val	Cys	Glu	Ser	Pro	Thr	Lys	
317					340			345			350						
319	ggc	ggc	cca	cga	cca	ctg	tat	cgt	gtg	cct	ccg	ttt	ccc	atc	cag	cat	1104
320	Gly	Gly	Pro	Arg	Pro	Leu	Tyr	Arg	Val	Pro	Pro	Phe	Pro	Ile	Gln	His	
321				355			360			365							
323	cta	cag	acc	ata	ttc	gcf	gtg	tcc	aag	aag	ctg	ctc	acc	aaa	gac	acc	1152
324	Leu	Gln	Thr	Ile	Phe	Ala	Val	Ser	Lys	Lys	Leu	Leu	Thr	Lys	Asp	Thr	
325	370				375			380									
327	ctc	qaa	cat	ctc	gac	qag	cag	gca	agc	gat	ata	ttt	tcg	ctg	cac	caa	1200
328	Leu	Glu	His	Leu	Asp	Glu	Gln	Ala	Ser	Asp	Ile	Phe	Ser	Leu	His	Gln	
329	385				390			395			400						
331	atc	aag	ggc	tat	tgc	tac	aag	agc	ttc	tcg	gaa	acg	ttg	aac	ctg	gtc	1248
332	Ile	Lys	Gly	Tyr	Cys	Tyr	Lys	Ser	Phe	Ser	Glu	Thr	Leu	Asn	Leu	Val	
333				405				410			415						
335	ctg	gtg	acc	ctg	ctc	agg	gaa	ctg	ctg	cag	cat	cag	gtt	gac	ctg	ccc	1296
336	Leu	Val	Thr	Leu	Leu	Arg	Glu	Leu	Leu	Gln	His	Gln	Val	Asp	Leu	Pro	
337				420			425			430							
339	acg	ccg	tgc	acc	aag	gat	gtg	cag	gag	ttc	gtc	aag	cgf	ctc	ttt	ctc	1344
340	Thr	Pro	Phe	Thr	Lys	Asp	Val	Gln	Glu	Phe	Val	Lys	Arg	Leu	Phe	Leu	
341		435				440			445								
343	aac	ggc	caa	acg	gag	ctg	cag	aat	aaa	cag	cag	gat	cag	gaa	cgf	gag	1392
344	Asn	Gly	Gln	Thr	Glu	Leu	Gln	Asn	Lys	Gln	Gln	Asp	Gln	Glu	Arg	Glu	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/22/2006  
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Input Set : N:\RJAVED\10527571.txt  
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**Please Note:**

~~Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.~~

Seq#:56; Xaa Pos. 415 ✓  
Seq#:57; Xaa Pos. 415  
Seq#:180; Xaa Pos. 551,572  
Seq#:181; Xaa Pos. 551,572  
Seq#:204; N Pos. 3000  
Seq#:204; Xaa Pos. 1000  
Seq#:205; Xaa Pos. 1000

### Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10527571.txt

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L:7030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:1248  
L:7202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:400  
L:27077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:180 after pos.:1680  
M:341 Repeated in SeqNo=180  
L:27254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:181 after pos.:544  
M:341 Repeated in SeqNo=181  
L:33762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:204 after pos.:2976  
M:341 Repeated in SeqNo=204  
L:34028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:992